An acetylation rheostat for the control of muscle energy homeostasis

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Abstract

In recent years, the role of acetylation has gained ground as an essential modulator of intermediary metabolism in skeletal muscle. Imbalance in energy homeostasis or chronic cellular stress, due to diet, aging, or disease, translate into alterations in the acetylation levels of key proteins which govern bioenergetics, cellular substrate use, and/or changes in mitochondrial content and function. For example, cellular stress induced by exercise or caloric restriction can alter the coordinated activity of acetyltransferases and deacetylases to increase mitochondrial biogenesis and function in order to adapt to low energetic levels. The natural duality of these enzymes, as metabolic sensors and effector proteins, has helped biologists to understand how the body can integrate seemingly distinct signaling pathways to control mitochondrial biogenesis, insulin sensitivity, glucose transport, reactive oxygen species handling, angiogenesis, and muscle satellite cell proliferation/differentiation. Our review will summarize the recent developments related to acetylation-dependent responses following metabolic stress in skeletal muscle.

Key Words
- acetylation
- sirtuins
- muscle adaptation
- oxidative metabolism
- glucose homeostasis

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The skeletal muscle is an essential organ for the maintenance of mobility and whole body metabolic health. The skeletal muscle demonstrates plasticity in mitochondrial content and function, vascular remodeling, glucose mobilization, and myogenesis/atrophy following metabolic stressors such as diet or exercise. As such, metabolic stress can have both acute and chronic effects on skeletal muscle homeostasis. Metabolic sensing is therefore a crucial component of skeletal muscle adaptation to various stressors and is imperative for whole body health.

This review will examine the essential metabolic sensing pathways that are regulated by posttranslational acetylation or deacetylation modifications that define the activity level and/or subcellular translocation of key proteins in muscle. Lysine-acetyltransferases (KATs; previously known as HATs) and -deacetylases (KDACs; also known as HDACs) regulate many proteins involved in intermediate metabolism (Guan & Xiong 2011, Patel et al. 2011), often by ‘sensing’ the redox state and/or the energetic state of the cell. These two states, although seemingly similar, describe different processes within the cell. The redox state often implies the NAD⁺:NADH or NADP⁺:NADPH ratio in a cell, which is correlated to the type of substrates being used to generate energy for the cell (Graham & Saltin 1989). The muscle cells that rely on glycolysis would typically be defined as having a lower NAD⁺:NADH ratio, while the myocytes that depend on...
fatty acid oxidation for energy production have a higher NAD\(^+\)/NADH quotient (Guarente 2012). Not so divergent from this description, but an important distinction, the energetic state of a muscle conveys the state of available energy to perform work, in the form of ATP, and yet is also inherently integrated with the redox state of a cell. Given that the muscle is a large organ, whole body energy homeostasis relies to a large extent on muscle mitochondrial function for aerobic ATP production and for the maintenance of physiological redox conditions. This reliance on muscle, in turn, can prevent insulin resistance which can predispose to obesity, diabetes, and cardiovascular disease, all of which contribute to accelerated aging (Patti et al. 2003, Joseph et al. 2012).

The known and potential roles of sirtuin proteins in muscle energy homeostasis

The sirtuin proteins (SIRT1–SIRT7) are a major subfamily of the KDACs. They have become increasingly regarded as the regulators of metabolism (reviewed in Guarente (2012) and Houtkooper et al. (2012)). In particular, the SIRT1 homolog has been identified as a metabolically regulated protein capable of sensing cellular redox status that can then illicit mitochondrial and redox defense adaptations (Cantó et al. 2012). SIRT2, a predominantly cytosolic protein, has not been studied in muscle but has been shown to regulate autophagy in mammalian cells (Zhao et al. 2010) and differentiation in adipocytes (Jing et al. 2007). Recent evidence has also linked SIRT2 with a potential role in cardiac protection from ischemic injury (Narayan et al. 2012). The mitochondrially located sirtuins, SIRT3, SIRT4, and SIRT5, are known to modulate the acetylation status of the mitochondrial proteins and may therefore directly influence muscle metabolism and stress responses (reviewed in Pirinen et al. (2012)). SIRT6 and SIRT7 are preferentially nuclear proteins. Of these nuclear proteins, SIRT6 expression is elevated with exercise and plays a role in glycolytic regulation that will be discussed further in this review (Koltai et al. 2010, Xiao et al. 2010). In contrast, SIRT7 has a low expression level in skeletal muscle, but it may play a role in cardiac muscle function and plasticity (Ford 2006). Although not discussed in this review, there is also recent evidence that non-sirtuin deacetylases can act as metabolic sensors and may regulate metabolism and other processes in a metabolite-sensitive manner that is dependent on changes in coenzyme A (CoA) derivatives as well as NADPH (Vogelauer et al. 2012).

Despite the recent surge in sirtuin research, there are still many questions to be answered concerning the influence of these energy-sensing proteins on muscle metabolism and homeostasis. Elucidation of sirtuin pathways will certainly lead to a better understanding of the metabolic response of muscle to exercise or degenerative processes brought about by physiological stressors such as disease, aging, or unhealthy diets.

The SIRT1 and AMPK nexus regulates metabolic-dependent acetylation

An understanding of the redox state and energetic state of muscle is important during any physiological condition because the balance of these states determines the coordinated response of various energy sensors/effectors to regain muscle homeostasis. For instance, during both aerobic exercise training and caloric restriction (CR), skeletal muscle bioenergetics is coordinated by metabolic-sensing proteins, which independently detect changes in both the ratio of redox and energetic metabolites/substrates, more specifically the NAD\(^+\)/NADH and AMP:ATP ratios. These redox- and energy-sensing proteins include NAD\(^+\)-dependent deacetylase sirtuin proteins (Imai et al. 2000), with our focus here being SIRT1, SIRT3, and SIRT6 (Houtkooper et al. 2010), and the AMP-activated protein kinase (AMPK; Hardie et al. 2012). These effector proteins are activated upon changes in the abundance of the corresponding metabolites NAD\(^+\) and AMP. The level of these metabolites depend on a complex series of energetic (Xiao et al. 2007, Hardie et al. 2012) and redox pathways (Cantó & Auwerx 2012, Mouchiroud et al. 2013), along with a reliance on the quantity, type, and location of available energy substrate stores.

During exercise, muscle requires an abundant supply of ATP to maintain the rapid cycling of crossbridges between actin and myosin and the oscillatory changes in intracellular Ca\(^{2+}\) between the extracellular space and the sarcoplasmic reticulum. In addition, during aerobic metabolism NADH is extensively used to transfer electron loads from intermediary substrates to the electron transport chain to synthesize ATP via oxidative phosphorylation (OXPHOS). It is therefore evident that both AMPK and SIRT1, as AMP- and NAD\(^+\)-sensors, are central for detecting energy stress situations during muscle metabolism.

It is through an interaction of SIRT1 and AMPK signaling pathways that muscle metabolism is tuned to adapt to the demands of energetic stress. Initial evidence demonstrating the similarity of these two effector proteins
was revealed in longevity studies. In particular, early Sir2p (the yeast SIRT1 homolog) studies suggested that this protein increased longevity in an NAD\textsuperscript{+}-dependent manner (Tissenbaum & Guarente 2001, Anderson et al. 2003, Lin et al. 2004). Lifespan extension also occurred in Caenorhabditis elegans overexpressing the AMPK\textsubscript{\textalpha} subunit (AAK 2) of the AMPK hetero-trimeric complex (Apfeld et al. 2004). During periods of energy deprivation, AMPK is responsible for the phosphorylation of many proteins, including metabolic enzymes, such as acetyl-CoA carboxylase (ACC) for fatty acid oxidation, or the peroxisome proliferator-activated receptor-\gamma coactivator 1\alpha (PGC-1\alpha), a coactivator for the transcription of nuclear encoded mitochondrial proteins (Winder et al. 2000, Nemoto 2005, Jager et al. 2007, Rodgers et al. 2008). During energy deprivation there is also a rise in the NAD\textsuperscript{+}:NADH ratio, which enables SIRT1 to deacetylate up to 13 potential acetyl-acceptor lysine sites on PGC-1\alpha, resulting in the activation of PGC-1\alpha (Nemoto 2005, Rodgers et al. 2005, Lin et al. 2006).

The integration of AMPK and SIRT1 signaling, and thus the connection between AMPK activity and regulation of protein acetylation, is evident in pharmacological experiments where AICAR, an activator of AMPK, was shown to induce SIRT1 deacetylase activity (Cantó et al. 2009, Gurd et al. 2011). Although not yet shown in the muscle, experiments performed in vivo and in vitro demonstrated that AMPK activation can lead to the dissociation of the inhibitor deleted in breast cancer 1 (DBC1) from SIRT1, resulting in its activation (Nin et al. 2012). Furthermore, CR of mice and glucose restriction of primary myoblasts both culminate in the AMPK-mediated induction of nicotinamide phosphoribosyltransferase (NAMPT) transcription (Fulco et al. 2008, Cantó et al. 2009), the rate-limiting enzyme that converts NAM to NAD\textsuperscript{+} (Revollo et al. 2004, Houtkooper et al. 2010). Elevations in NAMPT expression increases the NAD\textsuperscript{+}:NADH ratio (Preiss & Handler 1957, Kosaka et al. 1971, Biegnanski & Brenner 2004), thereby activating SIRT1 (Revollo et al. 2004, Hayashida et al. 2010), and thus providing a clear mechanistic link between the activation of AMPK and an increase in SIRT1 activity. Conversely, AMPK\textsubscript{\textalpha}3-KO animals have lower levels of NAD\textsuperscript{+}, NAMPT, and deacetylated PGC-1\alpha following exercise (Cantó et al. 2010). The evidence is therefore convincing that AMPK controls the activity of SIRT1. In a reciprocal manner, some evidence has demonstrated that SIRT1 can also control the activity of AMPK. Through the use of an inducible SIRT1-KO model, AMPK-directed stimulation of muscle mitochondrial biogenesis by resveratrol was shown to be dependent on SIRT1 (Price et al. 2012). In addition, human cultured myotubes that carry a point mutation in SIRT1 exhibit reduced AMPK activation (Biason-Lauber et al. 2013). Furthermore, glucose-induced changes in AMPK activity appear to depend on SIRT1 abundance or activity in liver cells (Suchankova et al. 2009). Therefore, it appears that these two pathways can be independently activated but may possess overlapping and potentiating properties.

### Positive regulation of acetyltransferases antagonizes the role of AMPK and SIRT1

Structural and functional studies have shown that many KATs exist as multisubunit enzymatic complexes that contain acetyl-CoA-binding domains and bromodomains. Notably, bromodomains are the only known protein modules that are able to recognize the specific lysine residues that are acetylated (Mujtaba et al. 2007). General control non-repressed protein 5 (GCN5) and P300/CREB-associated factor (PCAF) are members of the GCN5-related N-acetyltransferases (GNAT) family (Roth et al. 2001). Other important KAT families include P300/CREB (protein of 300 kDa and CREB-binding protein; Wang et al. 2008), MYST, named after its family members (MOZ, YBF2/SAS3, SAS2, and TIP60), and the steroid receptor coactivator (SRC) family that includes SRC1 (or NCOA1), SRC2 (TIF2, GRIP1, or NCOA2), and SRC3 (ACTR, RAC3, AIB1, P/CIP, or TRAM) (Chen et al. 1997, Onate et al. 1998). Of these KATs, GCN5, PCAF, P300/CREB, TIP60, SRC1, and SRC3 have been shown to immunoprecipitate with PGC-1\alpha (Puigserver et al. 1999, Liner et al. 2006, Coste et al. 2008), yet the inhibition PGC-1\alpha through acetylation has only been shown for GCN5 and its close homolog PCAF (Liner et al. 2006). GCN5 also acetylates and inactivates PGC-1\beta, another family member of the PGC-1 transcriptional co-activators (Kelly et al. 2009).

Various regulatory nodes have been examined that help to describe the activation or deactivation of the inhibitory GCN5/PGC-1\alpha interaction. One potential node includes the subcellular translocation of GCN5 to the cytosol to attenuate its interaction with nuclear PGC-1\alpha, as has been shown to occur with an acute bout of exercise (Philp et al. 2011). Second, the deacetylase SIRT6 unexpectedly induces PGC-1\alpha acetylation through the deacetylation and activation of GCN5 (Dominy et al. 2012). This effect is attenuated with overexpression of a deacetylase-inactive mutant form of SIRT6. However, this finding appears to be in theoretical contention to the observed increase of SIRT6 protein in muscle with...
exercise (Koltai et al. 2010) and the ability of SIRT6 to inhibit hypoxia inducible factor-1α (HIF-1α) leading to decreased glycolysis and activation of OXPHOS (Zhong et al. 2010). Furthermore, muscle cells from SIRT6-KO mice exhibit increased GLUT4 membrane translocation along with increased whole cell expression of GLUT1 (Xiao et al. 2010), thus supporting the role of SIRT6 in glycolysis. Third, GCN5 expression in skeletal muscle is increased by the transcriptional coactivator SRC3 (Coste et al. 2008). In line with this, germline SRC3-KO mice display increased mitochondrial function and improved glucose homeostasis and are protected against obesity. In addition, the expression of SRC3, like GCN5, is sensitive to fasting and high-fat diet (Coste et al. 2008). Fourth, CITED2 (CBP- and P300-interacting transactivator with glutamic acid- and aspartic acid-rich COOH-terminal domain 2) has been shown to disrupt the acetylation and inhibition of PGC-1α by GCN5 in hepatocytes (Sakai et al. 2012). Upon insulin activation of PI3K/AKT signaling, the interaction between CITED2 and GCN5 is attenuated, allowing for PGC-1α acetylation, while glucagon promotes CITED2 protein expression, releasing PGC-1α from the negative control of GCN5. Although the influence of CITED2 on GCN5/PGC-1α interaction in muscle has not been examined, CITED2 mRNA has been shown to decrease in muscle with insulin stimulation (Coletta et al. 2008). In addition, studies on mouse muscle myotubes demonstrated that CITED2 could block the effects of glucocorticoids on muscle cell atrophy. Lastly, as acetyltransferases require acetyl-CoA as a substrate for lysine acetylation, nuclear or cytosolic supplies of acetyl-CoA may regulate the activity of GCN5 or PCAF. During times of energy surplus, tricarboxylic acid cycle-derived citrate can be converted into acetyl-CoA by ATP citrate lyase, resulting in elevated nuclear and cytosolic acetyl-CoA, which have been shown to affect histone acetylation (Wellen et al. 2009). Analogous to this, increased levels of acetyl-CoA are postulated to also potentiate PGC-1α acetylation through GCN5 or PCAF, although experimental evidence for this last hypothesis is lacking at present (reviewed in Jeninga et al. (2010)).

Defining the exact signaling network that governs the activity of GCN5/PCAF in muscle function will require extensive future work, which should include the characterization of muscle-specific GCN5/PCAF single or double KO animals and potentially studies on model organisms, such as worms, which contain a single GCN5/PCAF homolog, pcaf-1.

The commanding role of the NAD⁺:NADH ratio in energy homeostasis

As a metabolic cofactor and a redox determinant, NAD⁺ is also required as an obligatory cosubstrate for sirtuin enzymes. The balance of the oxidized form (NAD⁺) vs the reduced form (NADH) dictates many of the functions of NAD⁺-dependant enzymes. In particular, the NAD⁺:NADH ratio influences the activity of redox reactions during the catabolism of lipids, proteins, carbohydrates, and alcohols. In addition, NAD⁺ has been shown to impact on glycolysis and OXPHOS and various fundamental regulatory functions, such as transcription, DNA repair, G-protein-coupled signaling, and intracellular calcium signaling (Bogan & Brenner 2008, Garten et al. 2009). With all of these essential biological functions relying on NAD⁺, the availability of NAD⁺ for sirtuin activity is limited (Rodgers et al. 2005, Sun et al. 2007, Bogan & Brenner 2008, Cantó et al. 2010, Hayashida et al. 2010, Koltai et al. 2010). NAD⁺ is derived from the amino acid tryptophan or from nicotinic acid or nicotinamide (NAM), which are biosynthesized de novo from vitamin B3 (Magni et al. 2004, Houtkooper et al. 2010, Schenk et al. 2011, Fernandez-Marcos et al. 2012). Interestingly, the NAD⁺ intermediate, nicotinamide mononucleotide (NMN), can restore NAD⁺ levels and improve glucose tolerance in high fat diet (HFD)-induced diabetic mice, when given via i.p. injection (Yoshino et al. 2011). Another NAD⁺ precursor is NAM riboside (NR; Rowen & Kornberg 1951), which, like NAM, can increase intracellular NAD⁺ levels via the NAD⁺ salvage pathway (Bieganowski & Brenner 2004). NR-supplemented diets have been shown to increase NAD⁺ levels and the activity of SIRT1 and SIRT3 in mice, culminating in enhanced skeletal muscle mitochondrial function (Cantó et al. 2012). Delivery of NR into mammalian cells occurs via nucleoside transporters, such as the equilibrative nucleoside transporters (ENT; Nikiforov et al. 2011). This was demonstrated through the use of the ENT inhibitors dipipyridamole or NBTI. It is therefore predicted that NR is delivered into muscle via ENT1, ENT2, and ENT3, which were shown to be expressed in the skeletal muscle (Lu et al. 2004).

As NAM can inhibit the different sirtuins (Bitterman 2002), the activity of the NAD⁺ salvage pathway becomes very important. The rate-limiting enzyme in the salvage pathway is the enzyme NAMPT. In fact, PNC1, the yeast ortholog of mammalian NAMPT, is essential for Sir2p-dependent lifespan extension during CR (Anderson et al. 2003). NAMPT most likely plays a key role in metabolism and potentially increases healthspan in mammals.
Evidence for the importance of NAMPT has been shown in cells deprived of glucose or serum (Yang et al. 2007) and in skeletal muscles of fasted mice (Fulco et al. 2008, Cantó et al. 2009). In addition, NAMPT expression is greatest in highly oxidative muscles and increases in expression with aerobic exercise training in both rats and humans (Costford et al. 2010, Koltai et al. 2010). These observations provide further evidence for the potential use of nutra- or pharmaceuticals to activate sirtuin-mediated deacetylation by enhancing the NAD⁺ salvage pathway or by introducing substrates for de novo biosynthesis of NAD⁺.

**Protein acetylation status in muscle affects substrate metabolism**

Skeletal muscle is highly reliant on substrates that drive OXPHOS activity. Lipids, which can be oxidized by mitochondria, are provided by lipolysis in adipose tissue and of intramuscular triacylglycerols. Carbohydrates, in the form of glucose, can be sequestered from the circulation in the post-prandial phase or following hepatic gluconeogenesis or glycolgenolysis. Alternatively, glucose can also be generated by intramuscular glycolgenolysis. Depending on exercise activity, muscle utilizes various energy stores ranging from glucose and glycogen to fats to synthesize ATP. As exercise intensity increases, there is a decrease in the proportion of energy derived from lipid oxidation and an increase in carbohydrate oxidation (reviewed in Graham & Saltin (1989), Holloszy et al. (1998), and Sahlin & Harris (2008)). Conversely, the proportion of energy derived from lipid oxidation rises significantly during prolonged exercise at low and moderate intensities.

Defects in human skeletal muscle mitochondria (Simoneau et al. 1995, Simoneau & Kelley 1997, Kelley et al. 2002, Ritov et al. 2005, Samjoo et al. 2013), reduced expression of OXPHOS genes (Mootha et al. 2003, Patti et al. 2003, Samjoo et al. 2013) and aberrant mitochondrial function and morphology (Kelley et al. 2002, Morino et al. 2005), all lead to the accumulation of intramyocellular lipids, which has been proposed as a potential mechanism leading to insulin resistance and diabetes. However, a recent study that examined the effects of endurance training in lean and obese men has found no definitive improvement in whole body insulin resistance despite reporting favorable mitochondrial adaptations and suggested that intramyocellular lipid profiles in obesity may only partially contribute to insulin resistance (Samjoo et al. 2013). Clearly, obesity-induced insulin resistance is a result of perturbations that go beyond mitochondrial biogenesis and intramyocellular lipid oxidation. As alterations in protein acetylation have strong influences on signaling pathways related to glucose homeostasis and insulin sensitivity, this posttranslational modification may contribute to these discrepancies. For example, the acetylation substrate acetyl-CoA, the product of both glucose and fatty acid breakdown, has been shown to influence mammalian cell histone acetylation, thus highlighting the link between acetylation and metabolism (Wellen et al. 2009). Although it needs to be confirmed that acetyl-CoA levels directly influence the acetylation of non-histone proteins, the fact that the deacetylation activity of SIRT1 improves insulin sensitivity in diet-induced obese mice, by activating PGC-1α amongst others, also suggests a link between protein acetylation levels and metabolism (Lagouge et al. 2006, Sun et al. 2007, Cantó et al. 2010). Furthermore, increased expression of SIRT1, or treatments with SIRT1 agonists, was shown to be similarly beneficial (Baur et al. 2006, Smith et al. 2009). Conforming to the involvement of SIRT1 in glucose homeostasis, cultured myotubes obtained from patients with SIRT1-L107P mutations exhibit both reduced glucose uptake and insulin sensitivity (Bisson-Lauber et al. 2013). The SIRT1-mediated effect on insulin resistance occurs, in part, through the deacetylase-dependent transcriptional repression of PTP1B at the chromatin level (Sun et al. 2007). As a key insulin receptor phosphatase, PTP1B can inhibit the insulin signaling transduction cascade. In addition, SIRT1 positively mediates CR-induced insulin sensitivity in muscle by deacetylating STAT3, thereby enhancing PI3K signaling and glucose uptake (Schenk et al. 2011). Therefore SIRT1 may not only increase β-oxidation of lipids through the activation of PGC-1α, but may also increase insulin sensitivity in a PTP1B- and STAT3-dependent manner to improve substrate handling during times of energy stress. SIRT1 may therefore be a potential target for the prevention or treatment of diabetes in humans through its insulin sensitization effects.

Contrary to the effects of SIRT1 deacetylase activity in the nucleus or cytosol, changes in mitochondrial protein acetylation, brought about by either liver- or muscle-specific SIRT3-KO animals, had no effect on metabolic homeostasis (Fernandez-Marcos et al. 2012). Despite this finding, germline SIRT3-KO mice exhibited both reduced hepatic and muscle fatty acid oxidation, along with reductions in hepatic ATP production, resulting in hypoglycemia, cold intolerance, and impaired insulin sensitivity (Hirschey et al. 2010, Jing et al. 2011). SIRT3 may also counterbalance mitochondrial acetylation induced by the GCN5-like 1 (GCN5L1) protein, as was shown to be the case in liver cells (Scott et al. 2012).
HIF-1α is an oxygen-sensitive protein that can facilitate ATP generation in mitochondrial respiration by inducing an angiogenic response that elevates VEGF expression to match the new demand of oxygen as a substrate for oxidative respiration (O’Hagan et al. 2009). HIF-1α induction of VEGF-A expression occurs with ischemic conditions in the heart and in skeletal muscles during exercise (Gustafsson et al. 1999, Ameln et al. 2005). With 4 days of chronic electrical stimulation of muscle, VEGF-A reaches its highest levels, while the capillary-to-muscle fiber ratio continually increases from 7- to 28-days of muscle stimulation (Dawson & Hudlicka 1989, Hudlicka & Price 1990, Hang et al. 1995). Interestingly, following PGC-1α overexpression in primary human skeletal muscle cells and the resulting induction of mitochondrial biogenesis, there is an increase in oxygen consumption, leading to intracellular hypoxia and the stabilization of HIF-1α (O’Hagan et al. 2009, Geng et al. 2010). However, PGC-1α can also directly regulate VEGF and angiogenesis in a HIF-1α-independent manner (Arany et al. 2008).

A sirtuin/HIF-1α balancing act: does SIRT1/SIRT6 mediate the metabolic switch from glycolysis to OXPHOS in muscle?

Although not examined in muscle, recent findings demonstrate that SIRT1 negatively regulates HIF-1α via deacetylation, while PCAF acetylates and activates the oxygen-sensitive protein (Lim et al. 2010). In addition, in mice and cells exposed to hypoxic conditions glycolysis is activated and the tricarboxylic acid cycle is inhibited, leading to decreases in NAD⁺ levels, reduced SIRT1 activity, and activation of HIF-1α. During normoxic conditions, NAD⁺ concentrations are higher resulting in SIRT1-mediated deacetylation and inactivation of HIF-1α (Lim et al. 2010). From this we hypothesize that HIF-1α may be inactivated by SIRT1 in muscle with exercise, as exercise has been shown to increase the NAD⁺:NADH ratio and SIRT1 activity (Graham & Saltin 1989, Cantó et al. 2009, 2010, Costford et al. 2010). As discussed in the previous section, exercise may result in a temporary hypoxic environment, much like what occurs with over-expression of PGC-1α, which would activate angiogenesis to supply the new demand for oxygen fueled by the increased mitochondrial content. Thus the induction of mitochondrial biogenesis following exercise could lead to intracellular hypoxia, leading to a reduction in OXPHOS activity, NAD⁺ availability, and the deactivation of SIRT1 and activation of HIF-1α by PCAF (see Fig. 1).
HIF-1α is also involved in cellular pathways related to glucose metabolism, such as glucose uptake and enzymes that regulate carbohydrate catabolism. Specifically, HIF-1α activates transcription of the glucose transporter 1, hexokinase 1 and 2, lactate dehydrogenase, pyruvate kinase, and other enzymes involved in glucose metabolism (reviewed in Semenza 2001). The balance between SIRT1 and HIF-1α regulation of the metabolic switch, going from oxidative to glycolytic metabolism, is corroborated by data showing reduced SIRT1 activity in muscles of aged rats and mice due to low NAD⁺ levels, leading to an increased dependence on glycolysis (Mouchiroud et al. 2013). The reduction in SIRT1 activity releases the inhibition of HIF-1α, which supports the increasing reliance of aged muscle on glycolysis for energy production (Koltai et al. 2010). Aged animals exhibit increases in lactate and reduced glycolytic intermediates suggesting elevated anaerobic glycolysis (Houtkooper et al. 2011). However, HIF-1α action is not just controlled by SIRT1, SIRT6 also inhibits HIF-1α and glucose uptake in muscle. Deficiency of the SIRT6 protein in skeletal muscle leads to severe hypoglycemia due to heightened HIF-1α activity and glucose uptake along with reduced mitochondrial respiration (Xiao et al. 2010). Under basal conditions, SIRT6 inhibits HIF-1α leading to decreased glycolysis and activation of OXPHOS (Zhong et al. 2010). Interestingly, SIRT6 expression increases with age in unison with HIF-1α and both proteins are reduced in these animals following exercise (Koltai et al. 2010). This may indicate that SIRT6 acts as a compensation mechanism during old age to limit HIF-1α overactivity.

We propose that SIRT1 and SIRT6 coordinate their functions to regulate HIF-1α, glucose uptake, and glycolysis in muscle. This concept has been demonstrated in macrophage precursors during an acute inflammatory response where the NAD⁺-dependent activation of SIRT1 and SIRT6, negative regulators of HIF-1α, was responsible for the activation of PGC-1α and the silencing of HIF-1α transcription respectively (Liu et al. 2012). As a result, the coordination between SIRT1 and SIRT6 induces a metabolic switch from glucose metabolism to fatty acid oxidation. Future research examining the coordination of SIRT1 and SIRT6, along with the acetyltransferases GCN5 or PCAF, will help to define the potential PGC-1α- and HIF-1α-directed metabolic switch upon changes in oxygen demands, exercise-induced mitochondrial biogenesis, and other adaptations to metabolic stress in skeletal muscle.

**Protein acetylation modulates muscle satellite cell fate**

In contrast to what occurs within a differentiated muscle cell, SIRT1 acts as a regulator of peripheral satellite cell...
proliferation in hypoxic conditions (Rathbone et al. 2009). Muscle satellite cells exposed to a hypoxic environment induce a SIRT1-mediated increase in cell cycle progression through the overall repression of cyclin-dependent kinase inhibitors, key regulators of G₁–S phase transitions. In addition, increase in the activity and expression levels of the basic helix–loop–helix (bHLH) factor MYOD marks the beginning of satellite cell activation and differentiation and is required for normal muscle regeneration (Megeney et al. 1996, Kanisicak et al. 2009). MYOD activity is controlled by multiple acetylation sites. Mice that express a mutant form of MYOD that replaces two specific lysine acetylation sites with arginine exhibit a delayed capacity for muscle regeneration in vivo (Duquet et al. 2006). In fact, the yield of myoblasts in MYOD mutant muscle was twofold higher than that found in WT animals, yet when placed under differentiation conditions, in vitro, there was a perturbed expression of early and late differentiation markers. MYOD can be deacetylated in the cell by a SIRT1-dependent mechanism. SIRT1 associates to PCAF/GCN5 and deacetylates PCAF and MYOD to inhibit differentiation (Fulco et al. 2003). From this, we can hypothesize that in satellite cells, SIRT1 acts to protect hypoxic muscle tissue by preparing the muscle for regeneration by activating the proliferation of muscle satellite cells. Concurrently, SIRT1 inhibits the differentiation of these satellite cells until the muscle is once again in a normoxic environment. Conversely, the acetylation of MYOD and activation of differentiation occur through CBP/300 and PCAF acetylation activity (Sartorelli et al. 1999, Polesskaya et al. 2000, Polesskaya & Harel-Bellan 2001).

More recently, the ability of PCAF to activate MYOD was confirmed using a PCAF-specific inhibitor, embelin, which blocked differentiation of myoblasts into myotubes (Modak et al. 2013). Furthermore, the nuclear corepressor SMRT (silencing mediator of retinoid acid and thyroid hormone receptor) has been shown to bind and stimulate the deacetylase activity of HDAC3 toward MEF2 and PCAF causing repression of myogenesis (Grégoire et al. 2007). Likewise, the SMRT homolog NCOR1 (nuclear corepressor 1) recruits HDAC1 to the bHLH region of MYOD to repress gene transcription (Bailey et al. 1999). Importantly, muscle-specific ablation of NCOR1 in mice demonstrated enhanced exercise endurance due to an increase in muscle mass and mitochondrial biogenesis (Yamamoto et al. 2011). With the loss of NCOR1 in vivo, there was an increase in the acetylation levels and activity of MEF2, a transcription factor that potentiates the muscle-inducing activity of myogenic bHLH proteins (Yamamoto et al. 2011). In opposition to SIRT1-, NCOR1-, and SMRT-regulation of MYOD, the coactivator PC4 has been shown to increase the expression of MYOD, along with the ability of this protein to stimulate muscle regeneration and myoblast differentiation (Micheli et al. 2011). PC4 directs the formation of a trimolecular complex of PC4, NF-κB, and HDAC3, which deacetylates NF-κB, an inhibitor of MYOD expression, and sequesters it to the cytosol.

These studies demonstrate that the chronological progression of deacetylase or acetyltransferase activity is important for satellite cell proliferation and differentiation. These studies also highlight the importance of the balance between these opposing enzymes when considering the development of new pharmacological approaches to activate muscle regeneration. Future studies should better define the progression and interconnections between each of the regulatory nodes of differentiation, specifically through SIRT1, PCAF/GCN5, NCOR1, and SMRT regulation of myogenic transcription factors such as MYOD and MEF2.

**Reversible acetylation for the control of atrophy and autophagy**

The ubiquitin–proteasome and autophagy–lysosome systems are the major proteolytic pathways that contribute to muscle wasting. The ubiquitin–proteasome system may account for up to 80% of the proteolysis during muscle wasting and is activated by the muscle-specific ubiquitin ligases ATROGIN1 and MURF1. Regulation of muscle wasting through the acetylation of NF-κB, C/EBPβ, and FOXO transcription factors was previously reported (Gutierrez et al. 2002, Chen & Greene 2003, Perrot & Rechler 2005). The acetylation of multiple sites on NF-κB by P300/CBP alters the capacity of NF-κB to bind DNA, induce its transcriptional activity, and interact with IκB inhibitors. The transcription factor C/EBPβ was shown to play a role in muscle wasting through studies on dexamethasone treatment. This synthetic glucocorticoid increases P300 binding and acetylation of C/EBPβ (Yang et al. 2005, Chamberlain et al. 2012). When active, C/EBPβ binds to a C/EBPβ-responsive cis-element in the atrogin1/MAFbx gene promoter (Zhang et al. 2011). In addition, the activation of FOXO3A in skeletal muscle causes the transcription of both the atrogin1 and mrf1 genes, followed by the induction of the atrophy program (Sandri et al. 2004, Sandri 2010, Senf et al. 2010). SIRT1 and P300 have been shown to regulate the balance between inhibition and activation of FOXO3A via deacetylation and acetylation respectively (Brunet et al. 2004, van der Horst et al. 2004, Motta et al. 2004). Interestingly, during glucose restriction...
of mouse C2C12 myotubes, FOXO3A was also shown to form a complex on mtDNA with SIRT3 and mitochondrial RNA polymerase, thus increasing mitochondrial protein expression and respiration in response to the CR-induced atrophic signal (Peserico et al. 2013).

Acetylation can also regulate the process of autophagy, as was demonstrated in the dual muscle-specific KO mouse of HDAC1 and HDAC2 (Moresi et al. 2012). These mice exhibit a progressive myopathy that is preceded by impaired autophagic flux, yet the mechanistic link still remains elusive. Furthermore, deacetylation by SIRT1 is important for activating the autophagy-related genes ATG5, ATG7, and ATG8 in an NAD⁺-dependent manner in mammalian cells (Lee et al. 2007). SIRT2 also appears to be involved in autophagy through the activation of FOXO1. In adipocytes, SIRT2 can bind and deacetylate FOXO1, a regulator of both muscle wasting and autophagy in mammalian cells (Lee et al. 2007, Zhao et al. 2010). During oxidative stress or serum starvation, FOXO1 is released by SIRT2, allowing for the deacetylation of FOXO1 and the induction of an autophagic response (Zhao et al. 2010). Therefore, as FOXO proteins regulate key pathways during sarcopenia and muscle disuse (Sandri et al. 2004, Senf et al. 2011), SIRT2 may prove to be an interesting new avenue to manipulate autophagy and atrophy signaling in skeletal muscle. In addition, P300, which is responsible for acetylating FOXO1 in vivo and in vitro, also acts as a coactivator to potentiate FOXO1 transactivation (Perrot & Rechler 2005).

Here we emphasize the role of protein acetylation in atrophy and muscle wasting, along with the role of autophagy as a selective process for clearing dysfunctional proteins and organelles (reviewed in Menzies & Hood (2012) and Sandri (2013)). The importance of examining the role of reversible acetylation in these processes is evident from a clinical standpoint and for the basic understanding of protein and organelle turnover that exists in muscle tissue.

Conclusions

In muscle, the balance between catabolism and anabolism, substrate utilization, and oxygenation are tightly interwoven. From this discussion it should be apparent that acetylation tightly regulates these processes in a concerted manner. As a result, the muscle cell can synchronize energy status and blood flow to changes in local muscle metabolism without compromising each of these processes or the host. With the current rise in the elderly population, there is an urgent need to understand the basic mechanisms of muscle homeostasis and to delineate each of these pathways in order to rationally tackle medical problems such as age-related loss of muscle function or glucose intolerance. In addition, much like what occurs with aging, pathologies such as muscular dystrophies, amyotrophic lateral sclerosis, diabetes, and cancer have also been defined by reductions in muscle mass, mitochondrial content and function, and the associated reduced capacity for adaptations to metabolic stress.

A better understanding of the involvement of reversible acetylation in mechanisms that underlie the pathogenesis of metabolic dysregulation has been the goal of many studies and is an important step for the development of new therapeutic approaches. Reversible acetylation orchestrates key regulatory mechanisms for both muscle and whole body metabolic homeostasis. It is apparent from the data presented here that in many cases acetylation or deacetylation cannot be simply categorized as activators or inhibitors of transcription, as once thought. These are complex systems that are context- and protein-specific. Therefore, a better understanding of these systems may offer promising approaches for pharmacological or lifestyle interventions (i.e. exercise) to modulate the activity of this integrated system, leading to the maintenance of mitochondrial content and function, energy and oxygen supply, and ultimately skeletal muscle health.

Declaration of interest

The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the review reported.

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